

YALE UNIVERSITY
OSBORN BOTANICAL LABORATORY
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RM March 3, 1947.

Dear Dr. Mather:

This should perhaps have been written as a postscript to my letter of the 8th ult., since certain remarks therein will have to be revised.

The results of the cross $B-P-X T-L-B_1-Lac-V^r$ do not support the map order $B_1; BM:Lac:V:P:TL$ which seemed to be suggested by the comparisons of the crosses $BM \times TLB_1V^r$ and $BM \times TPV^r$. The data are:

$B-P-T+L+B_1+Lac+V^s \times B+P+T-L-B_1-Lac-V^r$. (The P here does not recombine with P of TP).

	$-R$	$+R$	$-S$	$+S$
Prototrophs:	25	0	27	4

$B_1^- + B_1^+$
(these are types from B_1 plates.
 B_1^- ca 10X B_1^+)

	62	2	41	1
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$B^- + B^+$
(from B plates- but B^- not more than about 1/2 as frequent as B^+)

	74	10	69	12.
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must this be B_1^+ ?

Why is B- so frequent in this cross? It is not frequent in the other crosses.

There are two respects in which these data do not fit the map order assumed above:

1. $-S$ is much too frequent ✓
2. B^- is much too infrequent.

Why is B^- so infrequent in this cross?

However, these data are not fatal to the hypothesis of linear linkage, since the recombination value for V in the cross $BM \times TP$ may depend on the map order $BM-P-V-T$, on the assumption that the recombinations between V and T...P depend on two crossovers. The numerical data are not inconsistent with the theory (even in the absence of interference) particularly if T is to some extent to the right of L.

This gives a map:

ca $B_1 \dots BM \dots Lac \dots P \dots V \dots L-T$

In this cross then, the ~~known~~ crossovers required are:
Prototrophs: A.DE (A.D is $-S$; A.E is $-R$; D=E)
or A.B.C.DE A.B.C.D is $+S$; A.B.C.E is $+R$ //
 B_1^- : DE or B.C.DE B^- F.DE & F.A, C.DE ABC.DE

What does M, look like in this cross?

$-S$ A.B.D
 $-R$ A.B.E
 $+S$ C.E
 $+R$ C.R

~~V+T should be close together~~

It would not appear to be too worthwhile to attempt to make too precise estimations of absolute distances from such data as these until we learn more about the possibilities of interferences, which could certainly throw one wide of the mark.

Another approach to the problem of linearity has suggested itself, and I am working on it now.

It should be possible to find 'cross-over suppressor' stocks after intense irradiation. These would be presumably based on the occurrence of inversions. It should be a relatively simple matter to detect inversions covering region A of the map, since crosses involving such stocks could yield B_1 --but no prototrophs. (using, eg $BM \times TLB_1$.) If such can be found, one can also determine ^{whether} ~~while~~, if ~~any~~ ^{any} of the regions B,C,D, or E are involved; a group of such stocks could provide evidence as to the linear plotting of regions of suppressed interchange and thereby indicate the linearity of the gene arrangement. First, the inversions will have to be detected ~~found~~.

What news on the new addition of your 'Statistical Analysis?'

Sincerely,

Joshua Lederberg
Joshua Lederberg.)